

BC #6



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/031,355

DATE: 06/12/2002  
TIME: 12:05:28

Input Set : A:\PU3513USw Seq Listing.txt  
Output Set: N:\CRF3\06122002\J031355.raw

3 <110> APPLICANT: Glaxo Group Limited  
 4 Knick, Vincent C  
 5 Stimmel, Julie B  
 6 Thurmond, Linda M  
 8 <120> TITLE OF INVENTION: Antibody combination  
 10 <130> FILE REFERENCE: PU3513  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/031,355  
 C--> 13 <141> CURRENT FILING DATE: 2002-05-15  
 18 <160> NUMBER OF SEQ ID NOS: 16  
 20 <170> SOFTWARE: PatentIn Ver.. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 740  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (24)..(740)  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 37 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu  
 38 1 5 10  
 40 gta gca aca gct aca ggt gtc cac tcc gat att gtg atg act cag tct 101  
 41 Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Val Met Thr Gln Ser  
 42 15 20 25  
 44 cca ctc tcc ctg ccc gtc acc cct gga gag ccg gcc tcc atc tcc tgt 149  
 45 Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys  
 46 30 35 40  
 48 agg tct agt aag aat ctc ctg cat agt aat ggc atc act tat ttg tat 197  
 49 Arg Ser Ser Lys Asn Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr  
 50 45 50 55  
 52 tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc tat cag 245  
 53 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Ile Tyr Gln  
 54 60 65 70  
 56 atg tcc aac ctt gcc tca ggg gtc cct gac agg ttc agt agc agt gga 293  
 57 Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly  
 58 75 80 85 90  
 60 tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct gag gat 341  
 61 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp  
 62 95 100 105  
 64 gtt ggg gtt tat tac tgt gct caa aat cta gag att cct cgg acg ttc 389

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65 Val Gly Val Tyr Tyr Cys Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe  
66 110 115 120  
68 ggc caa ggg acc aag gtg gag atc aaa cgt acg gtg gct gca cca tct 437  
69 Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser  
70 125 130 135  
72 gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc 485  
73 Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala  
74 140 145 150  
77 tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta 533  
78 Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val  
79 155 160 165 170  
81 cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt 581  
82 Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser  
83 175 180 185  
85 gtc aca gag cag gac aag gac agc acc tac agc ctc agc agc acc 629  
86 Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr  
87 190 195 200  
89 ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc 677  
90 Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys  
91 205 210 215  
93 gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac 725  
94 Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn  
95 220 225 230  
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98 Arg Gly Glu Cys  
99 235  
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103 <211> LENGTH: 238  
104 <212> TYPE: PRT  
105 <213> ORGANISM: Artificial Sequence  
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113 1 5 10 15  
115 Val His Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val  
116 20 25 30  
118 Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn Leu  
119 35 40 45  
121 Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro  
122 50 55 60  
124 Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser  
125 65 70 75 80  
127 Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr  
128 85 90 95  
130 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys  
131 100 105 110  
133 Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Val

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134	115	120	125
136	Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro		
137	130	135	140
139	Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu		
140	145	150	155
142	Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn		160
143	165	170	175
145	Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser		
146	180	185	190
148	Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala		
149	195	200	205
151	Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly		
152	210	215	220
154	Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
155	225	230	235

159 <210> SEQ ID NO: 3  
 160 <211> LENGTH: 740  
 161 <212> TYPE: DNA  
 162 <213> ORGANISM: Artificial Sequence  
 164 <220> FEATURE:  
 165 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 168 <400> SEQUENCE: 3  
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 170 ttcgcaggcg tagactttgt gtttctcgta gtctgtttg ctcagcgtca gggtgctgct 120  
 171 gaggctgttag gtgctgtcct tgctgtcctg ctctgtgaca ctctcctggg agttaccgaa 180  
 172 ttggagggcg ttatccacct tccactgtac tttggcctct ctggataga agttattcag 240  
 173 caggcacaca acagagggcag ttccagatt caactgctca tcagatggcg ggaagatgaa 300  
 174 gacagatggt gcagccaccg tacgtttgat ctccacccctg gtcccttggc cgaacgtccg 360  
 175 aggaatctct agattttgag cacagtaata aaccccaaca tcctcagccct ccactctgct 420  
 176 gatttcagt gtaaaatctg tgcctgatcc actgctactg aacctgtcag ggaccctgaa 480  
 177 ggcaagggtt gacatctgat agatcaggag ctgtggagac tgcctggct tctgcaggta 540  
 178 ccaataacaaa taagtgtatgc cattactatg caggagatc ttactagacc tacaggat 600  
 179 ggaggccggc tctccagggg tgacggcgag ggagagtggaa gactgagtcg tcacaatatc 660  
 180 ggagtggaca cctgttagctg ttgctaccaa gaagaggatg atacagctcc atcccatgg 720  
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 184 <210> SEQ ID NO: 4  
 185 <211> LENGTH: 1418  
 186 <212> TYPE: DNA  
 187 <213> ORGANISM: Artificial Sequence  
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 190 <221> NAME/KEY: CDS  
 191 <222> LOCATION: (24)..(1418)  
 194 <220> FEATURE:  
 195 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 199 cgtaagcttc acagatcctc acc atg gga tgg agc tgt atc atc ctc ttt ctg 53  
 200 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu

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201	1	5	10	
203	gtg gca aca gct aca ggt gtc cac tcc cag gta cag cta gtg caa tca		101	
204	Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser			
205	15	20	25	
207	ggg cct gaa gtg aag aag cct ggg gcc tca gtg aaa gtt tcc tgc aag		149	
208	Gly Pro Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys			
209	30	35	40	
211	gct tct ggc tac acc ttc acc aac tat gga atg aac tgg gta agg cag		197	
212	Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln			
213	45	50	55	
215	gcg cct gga cag ggg ctt gag tgg atg ggg tgg ata aac acc tac act		245	
216	Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr			
217	60	65	70	
219	gga gag cca aca tat ggt gaa gat ttc aag gga cgg ttt gca ttc tct		293	
220	Gly Glu Pro Thr Tyr Gly Glu Asp Phe Lys Gly Arg Phe Ala Phe Ser			
221	75	80	85	90
223	cta gac aca tcc gcc agc aca gcc tat atg gag ctc agc tcg ctg aga		341	
224	Leu Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg			
225	95	100	105	
227	tcc gag gac act gca gtc tat ttc tgt gcg aga ttt ggt aac tac gta		389	
228	Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Phe Gly Asn Tyr Val			
229	110	115	120	
232	gac tac tgg ggt caa gga tca cta gtc act gtc tcc tca gcc tcc acc		437	
233	Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr			
234	125	130	135	
236	aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc aag agc acc tct		485	
237	Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser			
238	140	145	150	
240	ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa		533	
241	Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu			
242	155	160	165	170
244	ccg gtg acg gtg tgg aac tca ggc gcc ctg acc agc ggc gtg cac		581	
245	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His			
246	175	180	185	
248	acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc		629	
249	Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser			
250	190	195	200	
252	gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc		677	
253	Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys			
254	205	210	215	
256	aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag		725	
257	Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu			
258	220	225	230	
260	ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct		773	
261	Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro			
262	235	240	245	250
264	gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag		821	
265	Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys			
266	255	260	265	

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269	gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	869
270	Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
271	270 275 280	
273	gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	917
274	Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
275	285 290 295	
277	ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	965
278	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
279	290 305 310	
281	aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1013
282	Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
283	315 320 325 330	
285	tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1061
286	Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
287	335 340 345	
289	cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1109
290	Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
291	350 355 360	
293	gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1157
294	Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
295	365 370 375	
297	aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1205
298	Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
299	380 385 390	
301	atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1253
302	Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
303	395 400 405 410	
306	acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc	1301
307	Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser	
308	415 420 425	
310	aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca	1349
311	Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser	
312	430 435 440	
314	tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc	1397
315	Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
316	445 450 455	
318	ctc tcc ctg tct ccg ggt aaa	1418
319	Leu Ser Leu Ser Pro Gly Lys	
320	460 465	
323	<210> SEQ ID NO: 5	
324	<211> LENGTH: 465	
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326	<213> ORGANISM: Artificial Sequence	
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/031,355

DATE: 06/12/2002

TIME: 12:05:29

Input Set : A:\PU3513USw Seq Listing.txt

Output Set: N:\CRF3\06122002\J031355.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date